

<sup>46</sup>  
~~48~~ ~~47~~. A method according to claim ~~45~~ wherein one amino acid residue in the sub-sequence is mutated.

<sup>46</sup>  
~~49~~ ~~48~~. A method according to claim ~~45~~ wherein the sub-sequence is capable of being digested by a serine protease.

<sup>49</sup>  
~~50~~ ~~49~~. A method according to claim ~~48~~ wherein the sub-sequence has an amino acid sequence including the sequence: RAAAG.

<sup>50</sup>  
~~51~~ ~~50~~. A method according to claim ~~49~~ wherein the sub-sequence is mutated by replacing arginine in the sequence: RAAAG with alanine.

<sup>49</sup>  
~~52~~ ~~51~~. A method according to claim ~~48~~ wherein the sub-sequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 17 to 44.

<sup>52</sup>  
~~53~~ ~~52~~. A method according to claim ~~51~~ wherein the sub-sequence is mutated by replacing arginine in the sequence selected from the group of sequences shown in SEQ ID NOS: 17 to 44 with alanine.

<sup>49</sup>  
~~54~~ ~~53~~. A method according to claim ~~48~~ wherein the sub-sequence is capable of being digested by thrombin and has an amino acid sequence shown in SEQ ID NOS: 8 or 9.

<sup>49</sup>  
~~55~~ ~~54~~. A method according to claim ~~48~~ wherein the sub-sequence is capable of being digested by plasmin and has an amino acid sequence shown in SEQ ID NOS: 11 or 12.

<sup>49</sup>  
~~56~~ ~~55~~. A method according to claim ~~48~~ wherein the sub-sequence is capable of being digested by kallikrein.

<sup>56</sup>  
~~57~~ ~~56~~. A method according to claim ~~55~~ wherein the sub-sequence has an amino acid sequence shown in SEQ ID NOS: 9 or 10.

<sup>46</sup>  
~~58~~ ~~57~~. A method according to claim ~~45~~ wherein the sub-sequence is capable of being digested by a metalloproteinase.

<sup>58</sup>  
~~59~~ ~~58~~. A method according to claim ~~57~~ wherein the sub-sequence has an amino acid sequence including the sequence: ALAAA.

<sup>59</sup>  
~~60~~ ~~59~~. A method according to claim ~~58~~ wherein the sub-sequence is mutated by replacing alanine at any position in the sequence: ALAAA with another amino acid residue.

<sup>100</sup>  
~~61~~ ~~60~~. A method according to claim ~~59~~ wherein the sub-sequence is mutated by replacing the alanine which is N-terminal to leucine in the sequence: ALAAA with another amino acid.

<sup>58</sup>  
~~62~~ ~~61~~. A method according to claim ~~57~~ wherein the sub-sequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 45 to 70.

<sup>62</sup>  
~~63~~ ~~62~~. A method according to claim ~~61~~ wherein the sub-sequence is mutated by replacing alanine at any position in the sequence selected from the group of sequences shown in SEQ ID NOS: 45 to 70 with another amino acid residue.

<sup>63</sup>  
~~64~~ ~~63~~. A method according to claim ~~62~~ wherein the alanine that is replaced is N-terminal to leucine.

<sup>58</sup>  
~~65~~ ~~64~~. A method according to claim ~~57~~ wherein the sub-sequence is capable of being digested by gelatinase A or B.

<sup>65</sup>  
~~66~~ ~~65~~. A method according to claim ~~64~~ wherein the sub-sequence has an amino acid sequence shown in SEQ ID NO: 13.

~~67~~ ~~66~~. A method according to any one of claims <sup>46</sup>~~45~~ <sup>66</sup>~~65~~ wherein the tropoelastin is human tropoelastin.

~~68~~ ~~67~~. A method for enhancing the susceptibility of a tropoelastin to proteolysis comprising inserting a sub-sequence into the tropoelastin so that the susceptibility of the tropoelastin to proteolysis is enhanced.

~~69~~ ~~68~~. A method according to claim <sup>68</sup>~~67~~ wherein one sub-sequence is inserted.

~~70~~ ~~69~~. A method according to claim <sup>68</sup>~~67~~ wherein the inserted sub-sequence is capable of being digested with a serine protease.

<sup>10</sup>  
~~71~~ ~~70~~. A method according to claim <sup>10</sup>~~69~~ wherein the inserted sub-sequence has an amino acid sequence including the sequence: RAAAG.

~~72~~ ~~71~~. A method according to claim <sup>10</sup>~~69~~ wherein the inserted sub-sequence has an amino acid sequence selected from the group of sequences shown in SEQ ID NOS: 17 to 44.

~~73~~ ~~72~~. A method according to claim <sup>10</sup>~~69~~ wherein the inserted sub-sequence is capable of being digested by thrombin and has an amino acid sequence shown in SEQ ID NOS: 8 or 9.

~~74~~ ~~73~~. A method according to claim <sup>10</sup>~~69~~ wherein the inserted sub-sequence is capable of being digested by plasmin and has an amino acid sequence shown in SEQ ID NOS: 11 or 12.

<sup>70</sup>  
~~75~~ ~~74~~. A method according to claim ~~69~~ wherein the inserted sub-  
sequence is capable of being digested by kallikrein.

<sup>75</sup>  
~~76~~ ~~75~~. A method according to claim ~~74~~ wherein the inserted sub-  
sequence has an amino acid sequence shown in SEQ ID NOS: 9 or 10.

<sup>68</sup>  
~~77~~ ~~76~~. A method according to claim ~~67~~ wherein the inserted sub-  
sequence is capable of being digested by a metalloproteinase.

<sup>77</sup>  
~~78~~ ~~77~~. A method according to claim ~~76~~ wherein the inserted sub-  
sequence has an amino acid sequence including the sequence: ALAAA.

<sup>77</sup>  
~~79~~ ~~78~~. A method according to claim ~~76~~ wherein the inserted sub-  
sequence has an amino acid sequence selected from the group of sequences shown in  
SEQ ID NOS: 45 to 70.

<sup>77</sup>  
~~80~~ ~~79~~. A method according to claim ~~76~~ wherein the inserted sub-  
sequence is capable of being digested by gelatinase A or B.

<sup>80</sup>  
~~81~~ ~~80~~. A method according to claim ~~79~~ wherein the inserted sub-  
sequence has the amino acid sequence shown in SEQ ID NO: 13.

<sup>68</sup> <sup>81</sup>  
~~82~~ ~~81~~. A method according to any one of claims ~~67~~ to ~~80~~ wherein the  
tropoelastin is human tropoelastin.

~~83~~ ~~82~~. A peptidomimetic molecule comprising all or part of a peptide  
selected from the group consisting of KAPGVGGAF, RAAAGLG, RLSPELREGD,  
KAAQFGLVPGV, KSAKVAAKAQLRAA, RLSPELRE AND  
LAAAKAAKYGAA.

~~84~~ ~~83~~. A peptidomimetic molecule which has the sequence: H-Ala-Ala-Lys-Ala-Gln-Leu-Arg-Ala-Ala-Ala-Gly-Leu-Gly-Ala-OH or H-Ala-Ala-Lys-Ala-Gln-Leu-Arg-R-Ala-Ala-Ala-Gly-Leu-Gly-Ala-OH (where R = a reduced peptide bond).

~~85~~ ~~84~~. A peptidomimetic molecule which is a retro-inverso pseudo peptide which has the sequence: H-D-Ala-Gly-D-Leu-Gly-D-Ala-D-Ala-D-Ala-(R)-D-Arg-D-Leu-D-Gln-D-Ala-D-Lys-D-Ala-D-Ala-OH (where R = a reduced peptide bond) or H-D-Ala-Gly-D-Leu-Gly-D-Ala-D-Ala-D-Ala-D-Arg-D-Leu-D-Gln-D-Ala-D-Lys-D-Ala-D-Ala-OH.

~~86~~ ~~85~~. A peptidomimetic molecule which has the sequence H-Val-Pro-Gly-Ala-Leu-Ala-Ala-Ala-OH or H-Val-Pro-Gly-Ala-(R)-Leu-Ala-Ala-Ala-OH (where R = a reduced peptide bond).

*cont*  
*B,*  
~~87~~ ~~86~~. A peptidomimetic molecule which is a retro-inverso pseudo peptide which has the sequence: H-D-Ala-D-Ala-D-Ala-D-Leu-(R)-D-Ala-Gly-D-Pro-D-Val-OH (where R = a reduced peptide bond) or H-D-Ala-D-Ala-D-Ala-D-Leu-D-Ala-Gly-D-Pro-D-Val-OH.

~~88~~ ~~87~~. A method for enhancing the purification of a tropoelastin <sup>83</sup> comprising including a peptidomimetic molecule according to any one of claims ~~82~~ <sup>81</sup> to ~~86~~ <sup>85</sup> in a crude tropoelastin preparation which is being subjected to purification.

~~89~~ ~~88~~. A pharmaceutical composition comprising a peptidomimetic molecule according to any one of claims ~~82~~ <sup>83</sup> to ~~86~~ <sup>81</sup> and a pharmaceutically acceptable carrier.

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